Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently Amended) A method ~~of detecting metastatic melanoma cells in a patient~~ for melanoma prognosis, comprising:

(a) isolating nucleic acid from a biological sample obtained from ~~the~~ a melanoma patient, wherein the biological sample is associated with melanoma;

(b) amplifying nucleic acid targets~~, if present,~~ from a panel of marker genes, wherein the panel comprises GalNAcT, PAX3, or both; ~~and~~

(c) detecting the ~~presence or absence~~ levels of the nucleic acid targets; and

(d) predicting melanoma recurrence, disease-free survival, overall survival, or a combination thereof, based on the levels of the nucleic acid targets.

2. (Currently Amended) The method of claim 1 wherein the panel further comprises marker genes selected from a group consisting of MAGE-A3, MART-1, ~~MITF, TRP-2,~~ and Tyrosinase.

3. (Currently Amended) The method of claim 2 wherein the panel comprises a first combination of MAGE-A3, GalNAcT, MART-1, and PAX3; or a second combination of ~~MART-1, GalNAcT, MITF, and PAX3; a third combination of MART-1, TRP-2, GalNAcT, and PAX3; or a fourth combination of~~ Tyrosinase, MART-1, GalNAcT, and PAX3.

4. (Original) The method of claim 1 wherein the nucleic acid is mRNA and the nucleic acid targets are amplified using real-time reverse transcriptase polymerase chain reaction (qRT-PCR).

5. (Original) The method of claim 1 wherein the biological sample is selected from a group consisting of paraffin-embedded (PE) melanoma tissues, frozen lymph nodes, and PE lymph nodes.

6. (Original) The method of claim 1, wherein the biological sample is histopathologically negative for melanoma cells.

7. (Original) The method of claim 6, wherein histopathology of the biological sample is determined by hematoxylin and eosin staining or immunohistochemistry.

8-9. (Canceled)

10. (Currently Amended) The method of claim ~~9~~ 1, wherein the patient's prognosis is predicted for at least a three-year period following a removal of a primary tumor, sentinel lymphadenectomy (SLND), or both.

11. (Currently Amended) The method of claim ~~9~~ 1 further comprising a step of selecting a treatment regimen based on the patient's prognosis.

12-30. (Canceled)

31. (New) A method for detecting the expression of a panel of marker genes in a patient, comprising:

(a) obtaining a sentinel lymph node (SLN) sample from a melanoma patient, wherein the sample is histopathologically negative for melanoma cells;

(b) isolating nucleic acid from the sample;

(c) amplifying nucleic acid targets from a panel of marker genes, wherein the panel comprises GalNAcT, PAX3, or both; and

(d) detecting the levels of the nucleic acid targets.

32. (New) The method of claim 31 wherein the panel further comprises marker genes selected from a group consisting of MAGE-A3, MART-1, and Tyrosinase.

33. (New) The method of claim 32 wherein the panel comprises a first combination of MAGE-A3, GalNAcT, MART-1, and PAX3; or a second combination of Tyrosinase, MART-1, GalNAcT, and PAX3.